

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/ 500, 671
Source: PCT
Date Processed by STIC: 1-26-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/500,671

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics**
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 **Misaligned Amino**
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 **PatentIn 2.0**
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 **Skipped Sequences**
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 **Skipped Sequences**
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 **Use of n's or Xaa's**
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 **Invalid <213>**
Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence.
- 11 **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 **PatentIn 2.0**
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

RAW SEQUENCE LISTING

DATE: 01/26/2005

PATENT APPLICATION: US/10/500,671

TIME: 12:29:27

Input Set : D:\1392-10-18-2.ST25.txt

Output Set: N:\CRF4\01262005\J500671.raw

3 <110> APPLICANT: Sera, Takashi
 5 <120> TITLE OF INVENTION: Nuclear-Envelope and Nuclear-Lamina Binding Chimeras for
 6 Modulating Gene Expression
 8 <130> FILE REFERENCE: 109845-163
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/500,671
 C--> 10 <141> CURRENT FILING DATE: 2004-07-02
 10 <160> NUMBER OF SEQ ID NOS: 18
 12 <170> SOFTWARE: PatentIn version 3.2
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 25
 16 <212> TYPE: PRT
 17 <213> ORGANISM: Artificial
 19 <220> FEATURE:
 20 <223> OTHER INFORMATION: Zinc finger domain
 23 <220> FEATURE:
 24 <221> NAME/KEY: MISC_FEATURE
 25 <222> LOCATION: (2)..(5)
 26 <223> OTHER INFORMATION: Amino acids 2-5 are Xaa wherein Xaa = any amino acid, and up
 to
 27 two amino acids can be missing.
 29 <220> FEATURE:
 30 <221> NAME/KEY: MISC_FEATURE
 31 <222> LOCATION: (7)..(18)
 32 <223> OTHER INFORMATION: Xaa can be any amino acid
 34 <220> FEATURE:
 35 <221> NAME/KEY: MISC_FEATURE
 36 <222> LOCATION: (20)..(24)
 37 <223> OTHER INFORMATION: Amino acids 20-24 are Xaa wherein Xaa = any amino acid, and
 up to
 38 two amino acids can be missing.
 40 <400> SEQUENCE: 1
 W--> 42 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 43 1 5 10 15
 46 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
 47 20 25
 50 <210> SEQ ID NO: 2
 51 <211> LENGTH: 32
 52 <212> TYPE: PRT
 53 <213> ORGANISM: Artificial
 55 <220> FEATURE:
 56 <223> OTHER INFORMATION: Second zinc finger domain
 59 <220> FEATURE:
 60 <221> NAME/KEY: MISC_FEATURE
 61 <222> LOCATION: (1)..(3)

Does Not Comply
 Corrected Diskette Needed
 (pg. 5, 7)

62 <223> OTHER INFORMATION: Xaa can be any amino acid

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64 <220> FEATURE:
 65 <221> NAME/KEY: MISC_FEATURE
 66 <222> LOCATION: (5)..(8)
 67 <223> OTHER INFORMATION: Amino acids 5-8 are Xaa wherein Xaa = any amino acid, and up
 to
 68 two amino acids can be missing
 70 <220> FEATURE:
 71 <221> NAME/KEY: MISC_FEATURE
 72 <222> LOCATION: (10)..(14)
 73 <223> OTHER INFORMATION: Amino acid 15 is Z(-1) wherein Z(-1) = Arg, Lys, Gln, Asn,
 Thr,
 74 Met, Leu, Ile, Glu or Asp.
 76 <220> FEATURE:
 77 <221> NAME/KEY: misc_feature
 78 <222> LOCATION: (15)..(15)
 79 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 81 <220> FEATURE:
 82 <221> NAME/KEY: MISC_FEATURE
 83 <222> LOCATION: (16)..(16)
 84 <223> OTHER INFORMATION: Xaa can be any amino acid
 86 <220> FEATURE:
 87 <221> NAME/KEY: MISC_FEATURE
 88 <222> LOCATION: (17)..(17)
 89 <223> OTHER INFORMATION: Amino acid 17 is Z2 wherein Z2 = Ser, Arg, Asn, Gln, Thr,
 Val,
 90 Ala, Asp or Glu.
 92 <220> FEATURE:
 93 <221> NAME/KEY: MISC_FEATURE
 94 <222> LOCATION: (18)..(18)
 95 <223> OTHER INFORMATION: Amino acid 18 is Z3 wherein Z3 = His, Lys, Asn, Gln, Ser,
 Ala,
 96 Val, Thr, Asp, or Glu
 98 <220> FEATURE:
 99 <221> NAME/KEY: MISC_FEATURE
 100 <222> LOCATION: (19)..(20)
 101 <223> OTHER INFORMATION: Xaa can be any amino acid
 103 <220> FEATURE:
 104 <221> NAME/KEY: MISC_FEATURE
 105 <222> LOCATION: (21)..(21)
 106 <223> OTHER INFORMATION: Amino acid 21 is Z6 wherein Z6 = Arg, Lys, Gln, Asn, Thr,
 Tyr,
 107 Leu, Ile, Met, Glu or Asp.
 109 <220> FEATURE:
 110 <221> NAME/KEY: MISC_FEATURE
 111 <222> LOCATION: (23)..(27)
 112 <223> OTHER INFORMATION: Amino acids 23-27 are Xaa wherein Xaa = any amino acid, and
 up to
 113 two amino acids can be missing.
 115 <220> FEATURE:
 116 <221> NAME/KEY: MISC_FEATURE
 117 <222> LOCATION: (29)..(32)
 118 <223> OTHER INFORMATION: Xaa can be any amino acid
 120 <400> SEQUENCE: 2

W--> 122 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
123 1 5 10 15

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Output Set: N:\CRF4\01262005\J500671.raw

126 Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa
127 20 25 30
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 28
132 <212> TYPE: PRT
133 <213> ORGANISM: Artificial
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Zinc finger domain
139 <220> FEATURE:
140 <221> NAME/KEY: MISC_FEATURE
141 <222> LOCATION: (13)..(13)
142 <223> OTHER INFORMATION: Amino acid 13 is Z(-1) wherein Z(-1) = Arg, Lys, Gln, Asn,
Thr,
143 Met, Leu, Ile, Glu or Asp.
145 <220> FEATURE:
146 <221> NAME/KEY: MISC_FEATURE
147 <222> LOCATION: (15)..(15)
148 <223> OTHER INFORMATION: Amino acid 15 is Z2 wherein Z2 = Ser, Arg, Asn, Gln, Thr,
Val,
149 Ala, Asp or Glu.
151 <220> FEATURE:
152 <221> NAME/KEY: MISC_FEATURE
153 <222> LOCATION: (16)..(16)
154 <223> OTHER INFORMATION: Amino acid 16 is Z3 wherein Z3 = His, Lys, Asn, Gln, Ser,
Ala,
155 Val, Thr, Asp or Glu.
157 <220> FEATURE:
158 <221> NAME/KEY: MISC_FEATURE
159 <222> LOCATION: (19)..(19)
160 <223> OTHER INFORMATION: Amino acid 19 is Z6 wherein Z6 = Arg, Lys, Gln, Asn, Thr,
Tyr,
161 Leu, Ile, Met, Glu or Asp.
163 <400> SEQUENCE: 3
W--> 165 Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Xaa Ser Xaa Xaa
166 1 5 10 15
169 Leu Gln Xaa His Gln Arg Thr His Thr Gly Glu Lys
170 20 25
173 <210> SEQ ID NO: 4
174 <211> LENGTH: 5
175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial
178 <220> FEATURE:
179 <223> OTHER INFORMATION: peptide
181 <400> SEQUENCE: 4
183 Gly Gly Gly Gly Ser
184 1 5
187 <210> SEQ ID NO: 5
188 <211> LENGTH: 11
189 <212> TYPE: PRT
190 <213> ORGANISM: Human immunodeficiency virus
193 <220> FEATURE:
194 <221> NAME/KEY: MISC_FEATURE
195 <222> LOCATION: (1)..(11)

- see item #11 on
error
summary
sheet.
Invalid
Response

RAW SEQUENCE LISTING

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Input Set : D:\1392-10-18-2.ST25.txt

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196 <223> OTHER INFORMATION: HIV Tat protein domain
198 <400> SEQUENCE: 5
200 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
201 1          5          10
204 <210> SEQ ID NO: 6
205 <211> LENGTH: 9
206 <212> TYPE: DNA
207 <213> ORGANISM: Human immunodeficiency virus
210 <220> FEATURE:
211 <221> NAME/KEY: misc_feature
212 <222> LOCATION: (1)..(9)
213 <223> OTHER INFORMATION: HIV DNA Binding Domain
215 <400> SEQUENCE: 6
216 gcagaagcc
219 <210> SEQ ID NO: 7
220 <211> LENGTH: 19
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial
224 <220> FEATURE:
225 <223> OTHER INFORMATION: DNA target sequence
227 <400> SEQUENCE: 7
228 gtgtgggtga gtgagtgtg
231 <210> SEQ ID NO: 8
232 <211> LENGTH: 19
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial
236 <220> FEATURE:
237 <223> OTHER INFORMATION: DNA target sequence
239 <400> SEQUENCE: 8
240 ggggctgggg gcggtgtct
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 7
245 <212> TYPE: PRT
246 <213> ORGANISM: Simian virus 40
249 <220> FEATURE:
250 <221> NAME/KEY: MISC_FEATURE
251 <222> LOCATION: (1)..(7)
252 <223> OTHER INFORMATION: Peptide from SV40 large T antigen
254 <400> SEQUENCE: 9
256 Pro Lys Lys Lys Arg Lys Val
257 1          5
260 <210> SEQ ID NO: 10
261 <211> LENGTH: 16
262 <212> TYPE: PRT
263 <213> ORGANISM: Artificial
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Peptide, residues 43-58 of the Antennapeida homeodomain
protein
269 <220> FEATURE:
270 <221> NAME/KEY: MISC_FEATURE

```


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Input Set : D:\1392-10-18-2.ST25.txt

Output Set: N:\CRF4\01262005\J500671.raw

271 <222> LOCATION: (1)..(16)
 272 <223> OTHER INFORMATION: Peptide, residues 43-58 of the Antennapeida homeodomain protein

274 <400> SEQUENCE: 10

276 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys

277 1 5 10 15

280 <210> SEQ ID NO: 11

281 <211> LENGTH: 34

282 <212> TYPE: PRT

283 <213> ORGANISM: Herpes Simplex Virus

286 <220> FEATURE:

287 <221> NAME/KEY: MISC_FEATURE

288 <222> LOCATION: (1)..(34)

289 <223> OTHER INFORMATION: Residues 267-300 of the HSV VP22 protein

291 <400> SEQUENCE: 11

293 Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr

294 1 5 10 15

297 Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro

298 20 25 30

301 Val Glu

305 <210> SEQ ID NO: 12

306 <211> LENGTH: 11

307 <212> TYPE: PRT

308 <213> ORGANISM: Artificial

310 <220> FEATURE:

311 <223> OTHER INFORMATION: Basic peptide with cellular uptake activity

314 <220> FEATURE:

315 <221> NAME/KEY: MISC_FEATURE

316 <222> LOCATION: (1)..(11)

317 <223> OTHER INFORMATION: Basic peptide with cellular uptake activity

319 <400> SEQUENCE: 12

321 Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala

322 1 5 10

325 <210> SEQ ID NO: 13

326 <211> LENGTH: 9

327 <212> TYPE: PRT

328 <213> ORGANISM: Artificial

330 <220> FEATURE:

331 <223> OTHER INFORMATION: Basic peptide with cellular uptake activity, "R9"

333 <400> SEQUENCE: 13

335 Arg Arg Arg Arg Arg Arg Arg Arg Arg

336 1 5

339 <210> SEQ ID NO: 14

340 <211> LENGTH: 16

341 <212> TYPE: PRT

342 <213> ORGANISM: Artificial

344 <220> FEATURE:

345 <223> OTHER INFORMATION: D-penetratin peptide

348 <220> FEATURE:

349 <221> NAME/KEY: MISC_FEATURE

↑
 The type of errors shown exist throughout the sequence listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
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DATE: 01/26/2005
 TIME: 12:29:28

Input Set : D:\1392-10-18-2.ST25.txt
 Output Set: N:\CRF4\01262005\J500671.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24,
 Seq#:2; Xaa Pos. 1,2,3,5,6,7,8,10,11,12,13,14,15,16,17,18,19,20,21,23,24,25
 Seq#:2; Xaa Pos. 26,27,29,30,31,32
 Seq#:3; Xaa Pos. 13,15,16,19

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
 per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,7,8,10,12,13,14,15,16,17,18

VERIFICATION SUMMARY

DATE: 01/26/2005

PATENT APPLICATION: US/10/500,671

TIME: 12:29:28

Input Set : D:\1392-10-18-2.ST25.txt

Output Set: N:\CRF4\01262005\J500671.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3